

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:47 ; Search time 11 Seconds

(without alignments)

203.611 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRQVRHVLGIGLIVLNKLY.....FQEAFLFFLLKNPLTCS 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	60	21.2	111	1	YG2C_YEAST	P53245 saccharomyc
2	59	20.8	310	1	O2A4_HUMAN	O95047 homo sapien
3	56.5	20.0	153	1	TRPB_YEAST	P53342 saccharomyc
4	56.5	20.0	399	1	TRPB_BUCAP	P42391 buchnera ap
5	56	19.8	378	1	CKR7_MOUSE	P47774 mus musculu
6	55.5	19.6	363	1	YRU5_CAEEL	O09351 caenorhabdi
7	55.5	19.6	385	1	MDOC_ECOLI	P75920 escherichia
8	54.5	19.3	596	1	MKC7_YEAST	P53379 saccharomyc
9	54	19.1	633	1	YIJ2_YEAST	P40497 saccharomyc
10	53	18.7	230	1	ULI6_HCMVA	P16757 human cytom
11	53	18.7	265	1	AQP5_HUMAN	P55064 homo sapien
12	53	18.7	322	1	CGM2_SCHPO	P36613 schizosacch
13	53	18.7	386	1	ADTL_GOSHI	O22342 gossypium h
14	53	18.7	643	1	VP4B_VACCV	P06440 vaccinia vi
15	53	18.7	644	1	VP4B_VACCC	P20643 vaccinia vi
16	52.5	18.6	350	1	OSTG_YEAST	P48439 saccharomyc
17	52.5	18.6	492	1	TR11_FUSSP	O13317 fusarium sp
18	52.5	18.6	716	1	IKKE_HUMAN	Q14164 homo sapien
19	52.5	18.6	2670	1	YAO5_SCHPO	Q10105 schizosacch
20	52	18.4	337	1	PAHX_BOVIN	O18778 bos taurus
21	52	18.4	378	1	CKR7_HUMAN	P32248 homo sapien
22	52	18.4	487	1	C135_DROME	O9VGB5 drosophila
23	52	18.4	644	1	VP4B_VARY	P33818 variola vir
24	52	18.4	677	1	NCPR_CAVPO	P37039 cavia porce
25	52	18.4	692	1	PHSG_AQUAE	O66932 aquifex aeo
26	51.5	18.2	124	1	MUT7_BUCAI	P57298 buchnera ap
27	51.5	18.2	348	1	ADT2_YEAST	P18239 saccharomyc
28	51.5	18.2	1056	1	YNN2_YEAST	P53914 saccharomyc
29	51	18.0	367	1	YOL2_CAEEL	Q09291 caenorhabdi
30	51	18.0	1122	1	PHYA_ARATH	P14712 arabidopsis
31	51	18.0	1262	1	CYA5_RAT	O04400 rattus norv
32	51	18.0	1264	1	CYA5_RABIT	P40144 oryctolagus
33	51	18.0	2524	1	NOTC_XENLA	P21783 xenopus lae

34	50.5	17.8	286	1	YTCP_BACSU	P53561 bacillus su
35	50.5	17.8	305	1	ADT_KLULA	P49382 kluyveromyc
36	50.5	17.8	397	1	TRPB_BUCDN	O68428 buchnera ap
37	50.5	17.8	523	1	PRIM_BORBU	O51653 borrelia bu
38	50.5	17.8	1071	1	UBP7_YEAST	P40453 saccharomyc
39	50	17.7	338	1	PAHX_HUMAN	O14832 homo sapien
40	50	17.7	396	1	ARRS_XENLA	P51477 xenopus lae
41	50	17.7	411	1	MK08_RAT	P49185 rattus norv
42	50	17.7	427	1	MK09_HUMAN	P45983 homo sapien
43	50	17.7	447	1	GNTF_ECOLI	P39373 escherichia
44	50	17.7	606	1	NU5M_FELCA	P48921 felis silve
45	50	17.7	676	1	NCPR_HUMAN	P16435 homo sapien

ALIGNMENTS

RESULT 1
YG2C_YEAST STANDARD; PRT; 111 AA.
AC P53245;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 13.6 kDa protein in VHT1-ROM1 intergenic region.
GN YGR069W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
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CC or send an email to license@sib-sib.ch).
DR EMBL; Z72853; CAA97071.1;
DR SGD; S0003301; YGR069W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 27 47 POTENTIAL.
FT DOMAIN 36 47 POLY-PHE.
SQ SEQUENCE 111 AA; 13603 MW; 161DE34E1D75AAEA CRC64;
Query Match 21.2%; Score 60; DB 1; Length 111;
Best Local Similarity 34.0%; Pred. No. 0.63;
Matches 16; Conservative 5; Mismatches 20; Indels 6; Gaps 1;
QY 4 CVRHVLGIGLIVLNKLYPHKNSMPSPKLSSFQEAFLFFLLKNPL 50
Db 12 CTRYFL-----LLPSYTHPNHLFHPSPISFFFFFFFFFFFRNCL 52

RESULT 2
O2A4_HUMAN STANDARD; PRT; 310 AA.
ID O2A4_HUMAN
AC O95047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Olfactory receptor 2A4.
GN OR2A4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
 Hou S., Wohldmann P., Le T.;
 Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL: AC005587; AAD05193.1; -;
 DR Genew; HGNC:14729; OR2A4.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; FALSE_NEG.
 DR PROSITE; PS0362; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 25 48 1 (POTENTIAL).
 FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 57 78 2 (POTENTIAL).
 FT DOMAIN 79 99 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 100 119 3 (POTENTIAL).
 FT DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 139 157 4 (POTENTIAL).
 FT DOMAIN 158 194 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 195 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 258 6 (POTENTIAL).
 FT DOMAIN 259 271 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 272 291 7 (POTENTIAL).
 FT DOMAIN 292 310 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 310 AA; 34802 MW; 8C4F26BB855C8D7A CRC64;
 Query Match 20.8%; Score 59; DB 1; Length 310;
 Best Local Similarity 30.4%; Pred. No. 2.4;
 Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;
 QY 2 RCVRHVLTGLIVLKNLYFKNSMYPSPKLSFQEAFLFFLLKKNPL--TLCS 54
 Db 238 RTCFSLCIVGLVGTATIMVGRVGNPK---EQKKYLLLFHSLFNPMLNPLICS 290
 RESULT 3
 YG64_YEAST STANDARD; PRT; 153 AA.
 AC P53342;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Very hypothetical 17.3 kDa protein in MALIS-COS6 intergenic region.
 GN YG293C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=97245295; PubMed=9090054;
 RA Volckaert G., Voet M., Robben J.;
 RT "Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the
 RT right arm of chromosome VII from Saccharomyces cerevisiae carrying
 RT the MAL1 locus reveals 15 complete open reading frames, including
 RT ZUO1, BGL2 and BIO2 genes and an ABC transporter gene.";

RL Yeast 13:251-259(1997).
 [2]
 RN SEQUENCE OF 1-13 FROM N.A.
 RP Watson M.D.;
 RA Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: STRONG, TO YEAST YBR300C.
 CC
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 CC
 DR EMBL: Z73078; CAA97326.1; -;
 DR SGD: S0003525; YGR293C.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 1 21 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 SQ SEQUENCE 153 AA; 17314 MW; 75652655DBCC01E2 CRC64;
 Query Match 20.0%; Score 56.5; DB 1; Length 153;
 Best Local Similarity 27.0%; Pred. No. 2.5;
 Matches 17; Conservative 11; Mismatches 24; Indels 11; Gaps 2;
 QY 3 RCVRHV---LGIGLIVLKNLYFKNSM-----YSPKLSFQEAFLFFLLKKNPLT 51
 Db 74 QCSSHIHYSYVYGASVLCRCVFRHSRIRGARFIVPIFYCISKAQECFLTVYILPKNPF 133
 QY 52 LCS 54
 Db 134 VPS 136
 RESULT 4
 TRPB_BUCAP STANDARD; PRT; 399 AA.
 AC P42391;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tryptophan synthase beta chain (EC 4.2.1.20).
 GN TRPB.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94012512; PubMed=8407819;
 RA Munson M.A., Baumann P.;
 RT "Molecular cloning and nucleotide sequence of a putative trpDC(F)BA
 RT operon in Buchnera aphidicola (endosymbiont of the aphid Schizaphis
 RT graminum).";
 RL J. Bacteriol. 175:6426-6432(1993).
 CC -!- FUNCTION: THE BETA SUBUNIT IS RESPONSIBLE FOR THE SYNTHESIS
 CC OF L-TRYPTOPHAN FROM INDOLE AND L-SERINE.
 CC -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
 CC = L-tryptophan + glyceraldehyde 3-phosphate + H(2)O.
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TRPB FAMILY.
 CC
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DR EMBL; Z19055; CAA79500.1; -.
DR HSP; P00933; 2WSY.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000993; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
KW Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.
FT BINDING 86 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 399 AA; 42427 MW; DEBFD45D2C859C30 CRC64;

Query Match 20.0%; Score 56.5; DB 1; Length 399;
Best Local Similarity 36.2%; Pred. No. 6.4;
Matches 17; Conservative 9; Mismatches 12; Indels 9; Gaps 2;

QY 14 IVLKNLYFHKNMYPSPKLSFQEAFLFFLLILKN-----PLILCS 54
DB 19 ILMPALYOLEKNFVDKADSNFQKS---FFNLYKNYAGRPTPLILCN 62

RESULT 5
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7)
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
DE (EBI1).
GN CKR7 OR CMKBR7 OR EBI1 OR EBI1H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Rapoport C.J., Godiska R., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; L31580; AAA74232.1; -.
CC MGD; MGI:103011; Cmkbr7.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1.1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).

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FT TRANSMEM 239 259 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 311 331 POTENTIAL.
FT TRANSMEM 338 358 POTENTIAL.
SQ SEQUENCE 385 AA; 44690 MW; 248669CE8E0224DF CRC64;

Query Match 19.6%; Score 55.5; DB 1; Length 385;
Best Local Similarity 31.1%; Pred. No. 8.3;
Matches 14; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 8 VLIGLIVLKNLYFHKNMYPSPKLSFQDAFLFFLLIKNPLTL 52
   |||::: : : : : : : : : : : : : : : : : : :
Db 281 VLGLWMNVVFSFGHLLNFQSAVTVFVNASLFILV-HHPLTL 324

RESULT 8
MKC7_YEAST STANDARD; PRT; 596 AA.
ID MKC7_YEAST
AC P53379;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartic proteinase MKC7 precursor (EC 3.4.23.41) (Yapsin 2).
GN MKC7 OR YDR144C OR YD8358.01C OR YD2943.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96068694; PubMed=7479877;
RA Komano H., Fuller R.S.;
RT "Shared functions in vivo of a glycosyl-phosphatidylinositol-linked
RT aspartyl protease, Mkc7, and the proprotein processing protease Kex2
RT in yeast."
RL Proc. Natl. Acad. Sci. U.S.A. 92:10752-10756(1995).
RN [2]
RP SEQUENCE OF 1-196 FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 188-596 FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CLEAVES AT PAIRED BASIC RESIDUES. CAN PROCESS THE
CC ALPHA-MATING FACTOR PRECURSOR.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes various precursor proteins with Arg
CC or Lys in PL, and commonly Arg or Lys also in P2. The pI amino
CC acid is usually non-polar, but otherwise additional basic amino
CC acids are favorable in both non-prime and prime positions.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
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CC -----
CC EMBL; U14733; AAC49112.1; -
CC DR EMBL; Z50046; CAA90367.1; -
CC DR EMBL; Z54139; CAA90813.1; -
CC DR HSSP; P32329; 1YPS.
CC DR MEROPS; A01.031; -
CC DR SGD; S0002551; MKC7.
CC DR InterPro; IPR001461; Asprotease1.
CC DR InterPro; IPR001969; Asprotease_site.
CC DR Pfam; PF00026; asp; 1.

ID MDOC_ECOLI STANDARD; PRT; 385 AA.
AC P75920;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucans biosynthesis protein mdoc.
GN MDOC OR B1047.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=99296569; PubMed=10368134;
RA Lacroix J.-M., Lanfroy E., Cogez Y., Bohin A.,
RA Bohin J.-P.;
RT "The mdoc gene of Escherichia coli encodes a membrane protein that is
RT required for succinylation of osmoregulated periplasmic glucans."
RL J. Bacteriol. 181:3626-3631(1999).
CC -1- FUNCTION: NECESSARY FOR THE SUCCINYL SUBSTITUTION OF PERIPLASMIC
CC GLUCANS. COULD CATALYZE THE TRANSFER OF SUCCINYL RESIDUES FROM THE
CC CYTOPLASMIC SIDE OF THE MEMBRANE TO THE NASCENT GLUCAN BACKBONES
CC ON THE PERIPLASMIC SIDE OF THE MEMBRANE.
CC -1- PATHWAY: OPG (OSMOREGULATED PERIPLASMIC GLUCANS) BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: SOME, TO RHIZOBIUM NODULATION PROTEIN NOLL.
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CC -----
CC EMBL; AE000206; AAC74131.1; -
CC DR EMBL; D90741; BAA35837.1; -
CC DR EMBL; D90742; BAA35845.1; -
CC DR Ecogene; EG13876; mdoc.
CC Transmembrane; Complete proteome.
KW TRANSMEM 17 37 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.

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Query Match          19.1%; Score 54; DB 1; Length 633;
Best Local Similarity 41.0%; Pred. No. 21;
Matches 16; Conservative 4; Mismatches 15; Indels 4; Gaps 2;

QY      17  KNLVFKHNGMY-PSPKLSGSFQEAFLFFFLIL---KNPLT 51
      || ||| : ||| : ||| : ||| : ||| : |||
Dbb      286  KKNYFDKNSQHPDPARRKQNEPGMRLFLVMDEEKNILT 324

RESULT 10
ULI16.HCMVA
UL16.HCMVA          STANDARD;          PRT;          230 AA.
P16757:
DT      01-AUG-1990 (Rel. 15, Created)
DT      01-AUG-1990 (Rel. 15, Last sequence update)
DT      01-FEB-1991 (Rel. 17, Last annotation update)
DE      Hypothetical protein ULI16.
OS      Human cytomegalovirus (strain AD169).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
RN      [1]
SEQUENCE FROM N.A.
MEDLINE=90269039; PubMed=21613119;
Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
"Analysis of the protein-coding content of the sequence of human
cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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or send an email to license@isb-sib.ch).
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EMBL; X17403; CAA35448.1; -
PIR; S09778; S09778.
Hypothetical protein.
CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 230 AA; 26147 MW; B72F2C241C569967 CRC64;

Query Match          18.7%; Score 53; DB 1; Length 230;
Best Local Similarity 23.8%; Pred. No. 11;
Matches 15; Conservative 8; Mismatches 16; Indels 24; Gaps 2;

QY      15  VLKNIYFHKNMYP-----SPKLSGFQ-----AFLFFFLIKNPL 50
      ::: || : ||| : ||| : ||| : ||| : |||
Dbb      150  IIERLYVRGLSYPGPGSLAKHPSSVADELSATLARDIVLSAITIFFFLAIRPQ 209

      51 TLC 53
      ||
      210 RLC 212

RESULT 11
AOP5_HUMAN
AOP5_HUMAN          STANDARD;          PRT;          265 AA.
P55064:
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)

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Search completed: November 21, 2002, 13:41:50
Job time : 13 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:47 ; Search time 29 Seconds
(without alignments)
383.674 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRRCVRHVLGIGLIVLNKLY.....FQEAFLFFFLILKNPLTLC 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	22.3	395	10 Q9STW2	Q9stw2 arabidopsis
2	60	21.2	221	17 Q26431	Q26431 methanobact
3	59	20.8	272	4 Q9NQ00	Q9nq00 homo sapien
4	58.5	20.7	325	13 Q918C2	Q918c2 xenopus lae
5	58.5	20.7	612	10 Q24437	Q24437 oryza longi
6	58	20.5	401	10 Q82159	Q82159 populus nig
7	58	20.5	440	8 Q9BB39	Q9bb39 dichaea mur
8	58	20.5	446	8 Q9BBP4	Q9bbp4 pescatorea
9	58	20.5	452	8 Q9BB32	Q9bb32 pescatorea
10	58	20.5	457	8 Q9BB33	Q9bb33 chondrorrhyn
11	58	20.5	486	8 Q9BB38	Q9bb38 dichaea neg
12	58	20.5	559	5 Q24788	Q24788 echinococcu
13	58	20.5	795	5 Q8SS65	Q8ss65 encaphalito
14	57.5	20.3	170	16 Q8ZHG6	Q8zhg6 yersinia pe
15	57	20.1	503	8 Q9BB34	Q9bb34 cryptarhen
16	56.5	20.0	69	1 Q9C4Y2	Q9c4y2 sulfolobus

17	56.5	20.0	678	5	Q94736	Q94736 stomoxys ca
18	56.5	20.0	844	13	Q93552	Q93552 carassius a
19	56	19.8	119	8	Q8WF21	Q8wf21 bruntanitis
20	56	19.8	177	12	Q9YVZ0	Q9yvz0 metanopius
21	56	19.8	225	17	Q8THM5	Q8tht5 methanosarc
22	56	19.8	459	8	Q9BB37	Q9bb37 warrea warr
23	56	19.8	472	10	Q9LPL5	Q9lpl5 arabidopsis
24	56	19.8	472	10	Q9ZT57	Q9zt57 arabidopsis
25	56	19.8	491	16	Q8Y8L4	Q8y8l4 listeria mo
26	56	19.8	494	16	Q92DD2	Q92dd2 listeria in
27	56	19.8	604	2	Q9RMC9	Q9rme9 acinetobact
28	56	19.8	706	17	Q9YAG6	Q9yag6 aeropyrum p
29	55.5	19.6	217	8	Q9B601	Q9b6q1 eulachnus s
30	55.5	19.6	297	5	Q9XWR3	Q9xwr3 caenorhabdi
31	55.5	19.6	329	17	Q28580	Q28580 archaeoglob
32	55.5	19.6	345	4	Q96MA5	Q96ma5 homo sapien
33	55.5	19.6	385	16	Q8X9T6	Q8x9t6 escherichia
34	55.5	19.6	458	13	Q93555	Q93555 carassius a
35	55.5	19.6	1146	12	Q914N7	Q914n7 rice black
36	55.5	19.6	1146	12	Q8U209	Q8u209 rice black
37	55.5	19.6	2295	12	Q91TP1	Q91tp1 tupaiia herp
38	55	19.4	510	8	Q9BAZ7	Q9baz7 soteriosanth
39	55	19.4	510	8	Q9BAZ5	Q9baz5 kegeliiella
40	55	19.4	510	8	Q9BAZ4	Q9baz4 kegeliiella
41	55	19.4	769	10	Q9LHM0	Q9lhm0 arabidopsis
42	54.5	19.3	379	10	Q49447	Q49447 arabidopsis
43	54.5	19.3	441	2	Q34007	Q34007 staphylococ
44	54.5	19.3	675	5	Q9N5T3	Q9n5t3 caenorhabdi
45	54.5	19.3	1757	11	Q70481	Q70481 mus musculu

ALIGNMENTS

RESULT 1

Q9STW2	PRELIMINARY;	PRT;	395 AA.
ID	Q9STW2		
AC	Q9STW2;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	Hypothetical 45.7 kDa protein.		
GN	T22A6.150 OR A74G24320.		
OS	Arabidopsis thaliana (Mouse-ear cross).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I.,		
RA	Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	EU Arabidopsis sequencing project;		
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,		
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	EU Arabidopsis sequencing project;		
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL078637; CAB45067.1; -		
DR	EMBL; AL0161561; CAB79342.1; -		
DR	InterPro; IPR002203; Intein.		
DR	PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 395 AA; 45690 MW; EA8CE0F161E1E806D CRC64;		

EMBL: AL135904; CAB99212.1; -.
 InterPro: IPR000276; GPCR_Rhodopsn.
 Pfam: PF00001; 7tm_1; 1.
 PRINTS; PR00237; GPCRHHODOPS.
 PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
 NON_TER 1
 SEQUENCE 272 AA; 30452 MW; 4FFSCF18077574CD CRC64;

Query Match 20.8%; Score 59; DB 4; Length 272;
 Best Local Similarity 30.4%; Pred. No. 9.2;
 Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVRHVLGIGLVLKLYFHKNMYPSPKLSLSSQFAFLFFFLILKKNPL---TLCS 54
 DB 200 RCFCSHLCVGLVGTATIMVGVPRYGNPK---EQKKYLLLFHSLFNLPLNPLICS 252

RESULT 4
 Q918C2 PRELIMINARY; PRT; 325 AA.
 AC Q918C2;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 GN XB242.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OLFACTORY EPITHELIUM;
 RA Mezler M., Breer H.;
 RT "Two classes of olfactory receptors: molecular and functional studies.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250752; CAC00723.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 325 AA; 37075 MW; 94CDE3DC322C97A4 CRC64;

Query Match 20.7%; Score 58.5; DB 13; Length 325;
 Best Local Similarity 28.3%; Pred. No. 13;
 Matches 15; Conservative 7; Mismatches 28; Indels 3; Gaps 1

QY 4 CVRHVLGIGLVLKLYFHKNMYP---SPKLSLSSQFAFLFFFLILKKNPLTLCS 53
 DB 244 CTHLLVGLGYFIPRLFYVSTSQIPLIPDLNVLICLYTFPHLSPFIIC 296

RESULT 5
 Q24437 PRELIMINARY; PRT; 612 AA.
 AC Q24437;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Receptor kinase-like protein.
 OS Oryza longistaminata (Long-staminata rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
 OC Euryotata; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae;
 OX NCBI_TaxID=4528;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IRBB21;
 RX MEDLINE=96106403; PubMed=8525370;

RA Song W.Y., Wang G.L., Chen L.L., Kim H.S., Pi L.Y., Holsten T.,
 RA Gardner J., Wang B., Zhai W.X., Zhu L.H., Fauquet C., Ronald P.,
 RT "A receptor kinase-like protein encoded by the rice disease resistance
 RL gene, Xa21";
 RN Science 270:1804-1806(1995).
 RP [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=IRBB21;
 RX MEDLINE=97432142; PubMed=9286106;
 RA Song W.Y., Pi L.Y., Wang G.L., Gardner J., Holsten T., Ronald P.C.;
 RT "Evolution of the rice Xa21 disease resistance gene family";
 RL Plant Cell 9:1279-1287(1997).
 DR EMBL; U72726; AAB82753.1; -;
 DR InterPro: IPR001611; LRR;
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: PF00560; LRR; 21.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00370; LRR; 17.
 KW Kinase.
 SQ SEQUENCE 612 AA; 66380 MW; 9BE54BBB4242A91F CRC64;
 Query Match 20.7%; Score 58.5; DB 10; Length 612;
 Best Local Similarity 38.3%; Pred. No. 23;
 Matches 18; Conservative 5; Mismatches 19; Indels 5; Gaps 2;
 QY 1 MRCVRHVIGLIVLKNLYFKNSM---YFSP--KLSSFOEAFLEFF 42
 Db 163 LRGMIPREIGASIKHLNLYLHKNLSGEISALGNLTSLQFDFLSF 209
 RESULT 6
 ID 082159 PRELIMINARY; PRT; 401 AA.
 AC 082159;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Phosphoglycerate kinase (EC 2.7.2.3).
 GN PNCYTPGK2.
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nishiguchi M.;
 RT "A cDNA clone encoding cytosolic phosphoglycerate kinase 2 from
 RL Lombardy poplar";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-
 CC PHOSPHO-D-GLYCEROL PHOSPHATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
 DR EMBL; AB018411; BAA33802.1; -;
 DR HSSP; P18912; IHPH.
 DR InterPro: IPR001576; PGK.
 DR Pfam: PF00162; PGK; 1.
 DR PRINTS: PR00477; PGLYCKKINASE.
 DR PROSITE; PS00111; PGLYCERATE_KINASE; 1.
 KW Glycolysis; Kinase; Transferase.
 SQ SEQUENCE 401 AA; 42669 MW; 79B095EE6B1A9DA1 CRC64;
 Query Match 20.5%; Score 58; DB 10; Length 401;
 Best Local Similarity 29.5%; Pred. No. 18;
 Matches 13; Conservative 11; Mismatches 16; Indels 4; Gaps 1;
 QY 1 MRCVRHVIGLIVLKNLYFKNSMYPSP---KLSSFOEAFLE 40
 Db 103 KEKLVAEIPGGVLLNFRFHEEKNDEPAKLAIAEVIV 146
 RESULT 7

Q9BB39
 ID Q9BB39 PRELIMINARY; PRT; 440 AA.
 AC Q9BB39;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Probable intron maturase (Maturase K) (Fragment).
 GN MATK.
 OS Dichaea muricata.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
 OC Dichaea.
 OX NCBI_TaxID=125110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Whitten M., Williams N.H., Chase M.W.;
 RT "Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with
 RL special emphasis on Stanhopeinae: Combined molecular evidence.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
 CC INTRONS (BY SIMILARITY).
 CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
 CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
 CC MITOCHONDRIAL INTRONS.
 DR EMBL; AF239415; AAK31812.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
 KW Chloroplast; mRNA processing.
 FT NON_TER 1
 FT NON_TER 440 440
 SQ SEQUENCE 440 AA; 52685 MW; CFFBAF87755FF9E5 CRC64;
 Query Match 20.5%; Score 58; DB 8; Length 440;
 Best Local Similarity 29.6%; Pred. No. 20;
 Matches 16; Conservative 11; Mismatches 13; Indels 14; Gaps 2;
 QY 13 LIVLKNLYFKNSMYPSP-----PKLSSFOEAFLEFFLILKNPLPL 52
 Db 262 LILMKKWFHLVNFQSYFHFWFOPYRIHIKLPNYSFSLGYFSLVKNPLVV 315
 RESULT 8
 ID Q95BP4 PRELIMINARY; PRT; 446 AA.
 AC Q95BP4;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Probable intron maturase (Maturase K) (Fragment).
 GN MATK.
 OS Pescatorea lehmannii.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
 OC Pescatorea.
 OX NCBI_TaxID=125160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Williams N.H., Chase M.W., Fulcher T., Whitten M.W.;
 RT "Molecular systematics of the Oncidiinae based on evidence from four
 RL DNA sequence regions: expanded circumscriptions of Cyrtochilum,
 RL Erycina, Otaglossum, and Trichocentrum, and a new genus
 RL (Orchidaceae)";
 RL Lindleyana 16:113-139(2001).
 CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
 CC INTRONS (BY SIMILARITY).

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AC Q9BB33:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable intron maturase (Maturase K) (Fragment).
GN MATK.
OS Chondrorhyncha reichenbachiana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
OC Chondrorhyncha.
ON NCBI_TaxID=125095;
RX [1]
RN SEQUENCE FROM N.A.
RP Whitten M., Williams N.H., Chase M.W.;
RA "Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with
RT special emphasis on Stanhopeinae: Combined molecular evidence.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
CC EMBL; AF239421; AAK31813.1; -.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF01824; MatK_N; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN-1.
DR Chloroplast; mRNA processing.
KW NON_TER
FT NON_TER 457
FT NON_TER 457
SQ SEQUENCE 457 AA; 54601 MW; 06B18D9267078E9F CRC64;

Query Match , 20.5%; Score 58; DB 8; Length 457;
Best Local Similarity 29.6%; Pred. No. 20;
Matches 16; Conservative 11; Mismatches 13; Indels 14; Gaps

QY 13 LIVLKNLYFHKNWSPS-----PKLSFQEAFL-FFFLIKNPLTL 52
||:| || : : | || : : || : : ||||| :
DB 273 LILMKKFKHLVFWQSFHFQPYRIHKKLPNYSFGLGYFSLVKNPLVV 326

RESULT 11
Q9BB38 PRELIMINARY; PRT; 486 AA.
AC Q9BB38;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable intron maturase (Maturase K) (Fragment).
GN MATK.
OS Dichaea neglecta.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
OC Dichaea.
ON NCBI_TaxID=125111;
RX [1]
RN SEQUENCE FROM N.A.
RP Whitten M., Williams N.H., Chase M.W.;
RA "Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with
RT special emphasis on Stanhopeinae: Combined molecular evidence.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
CC INTRONS (BY SIMILARITY).
CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
CC MITOCHONDRIAL INTRONS.
CC EMBL; AF239416; AAK31813.1; -.

```

RC	STRAIN=GB-M1;
RA	Genoscope;
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RR	STRAIN=GB-M1;
RX	Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,
RY	Prensier G., Barbe V., Peyretallade E., Brottier P., Wincker P.,
RA	Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA	Weissenbach J., Vivares C.P.;
RT	"Genome sequence and gene compaction of the eukaryote parasite
RT	Encephalitozoon cuniculi.";
RL	Nature 414:450-453(2001).
DR	EMBL: AL590444; CAD25218.1; -
SQ	SEQUENCE 795 AA; 89126 MW; 6654367B915F89S16 CRC64;
Query Match	20.5%; Score 58; DB 5; Length 795;
Best Local Similarity	31.5%; Pred. No. 34;
Matches 17; Conservative 6; Mismatches 11; Indels 20; Gaps	
OY	9 LGIGLVILKNLYFHKNSWYP-----SPKLSSSQEAFLEFFFL 44 : : 671 LKGGLISIPLEYDKTFMPKNTIGLFSTVFMLLDSSISPLVSS--HAYMFLL 722
Ddb	
RESULT 14	
ID	PRELIMINARY; PRT; 170 AA.
AC	Q82HG6;
DT	01-MAR-2002 (TREMBlrel. 20, Created)
DD	01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	Hypothetical protein YPO0932.
GN	YPO0932.
OS	Yersinia pestis.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX	Yersinia.
NCBI_TaxID=632;	
[1]	
SEQUENCE FROM N.A.	
RC	STRAIN-CO-92 / BIOVAR ORIENTALIS;
RR	MEDLINE=21470413; PubMed=11586360;
RX	Parikhll J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RY	Prentice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,
RA	Baker S., Basham D., Bentley A.S., Davies R.K., Cerdeno-Tarraga A.M.,
RA	Chillingworth T., Cronin A., Brooks K., Churcher C., Mungall K.L.,
RA	Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA	Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA	Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT	"Genome sequence of Yersinia pestis, the causative agent of plague".
RT	Nature 413:523-527(2001).
RLL	Nature 413:523-527(2001).
DR	EMBL: AJ414145; CAC89775.1; -
DDR	InterPro: IPR000130; Zn_MTpeptidse.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.	
HHW	Hypothetical protein; Complete proteome.
SQ	SEQUENCE 170 AA; 19923 MW; 5C172226B3962FB90 CRC64;
Query Match	20.3%; Score 57.5; DB 16; Length 170;
Best Local Similarity	30.4%; Pred. No. 9.4;
Matches 17; Conservative 8; Mismatches 18; Indels 13; Gaps	
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Ddb	
RESULT 15	
ID	PRELIMINARY; PRT; 503 AA.
AC	Q9BB34;
DT	01-JUN-2001 (TREMBlrel. 17, Created)
DD	01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT	

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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:41:36 ; Search time 142 Seconds
(without alignments)
245.180 Million cell updates/sec

Title: US-09-776-724A-142
Perfect score: 283
Sequence: 1 MRRCVRHVLGIGLIVLNKLY.....FQEAFLFFLLKKNPLTICS 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues 4569144
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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27:	/cgn2_6/ptodata/1/paa/US60_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	54	1	PCT-US98-14613-142
2	283	100.0	54	16	US-09-229-982-142
3	283	100.0	54	20	US-09-659-688-142
4	283	100.0	54	21	US-09-776-724A-142
5	73	25.8	85	1	PCT-US01-01334-6555
6	73	25.8	85	21	US-09-764-874-6555

7	64.5	22.8	132	22	US-09-809-391-362	Sequence 362, App
8	64.5	22.8	132	22	US-09-882-171-362	Sequence 362, App
9	64.5	22.8	132	25	US-10-164-861-362	Sequence 362, App
10	64	22.6	89	1	PCT-US01-01330-164	Sequence 164, App
11	64	22.6	89	1	PCT-US01-01330-218	Sequence 218, App
12	64	22.6	89	1	PCT-US01-01339-4675	Sequence 4675, App
13	64	22.6	89	1	PCT-US01-01339-5353	Sequence 5353, App
14	64	22.6	89	21	US-09-764-891-4675	Sequence 4675, App
15	64	22.6	89	21	US-09-764-891-5353	Sequence 5353, App
16	63	22.3	260	21	US-09-708-427-29014	Sequence 29014, App
17	63	22.3	371	27	US-09-708-427-29013	Sequence 11072, App
18	63	22.3	395	21	US-09-708-427-29013	Sequence 29013, App
19	63	22.3	605	23	US-09-935-625-9687	Sequence 9687, App
20	63	22.3	605	23	US-09-935-625-9686	Sequence 9686, App
21	63	22.3	722	23	US-09-935-625-9686	Sequence 9686, App
22	63	22.3	722	23	US-09-935-625-9685	Sequence 9685, App
23	63	22.3	869	23	US-09-935-625-9685	Sequence 9685, App
24	63	22.3	869	23	US-09-935-625-9685	Sequence 9685, App
25	61	21.6	327	18	US-09-417-507-39964	Sequence 39964, App
26	60	21.2	165	18	US-09-417-507-39964	Sequence 39964, App
27	60	21.2	221	21	US-09-791-537-35767	Sequence 35767, App
28	59.5	21.0	237	19	US-09-513-996A-59523	Sequence 59523, App
29	59.5	21.0	251	19	US-09-513-996A-59522	Sequence 59522, App
30	59.5	21.0	307	19	US-09-513-996A-59521	Sequence 59521, App
31	59	20.8	93	27	US-60-196-713-3521	Sequence 3521, App
32	59	20.8	136	27	US-60-178-308-2457	Sequence 2457, App
33	59	20.8	197	27	US-60-163-232-1483	Sequence 1483, App
34	59	20.8	197	27	US-60-169-842-3895	Sequence 3895, App
35	59	20.8	260	21	US-09-761-288-35	Sequence 35, Appl
36	59	20.8	260	21	US-09-761-288-36	Sequence 36, Appl
37	59	20.8	260	22	US-09-898-586-35	Sequence 35, Appl
38	59	20.8	260	22	US-09-898-586-36	Sequence 36, Appl
39	59	20.8	272	23	US-09-907-218-35	Sequence 35, Appl
40	59	20.8	304	1	PCT-US00-34983B-58	Sequence 58, Appl
41	59	20.8	304	21	US-09-729-739-58	Sequence 58, Appl
42	59	20.8	304	21	US-09-747-835A-58	Sequence 58, Appl
43	59	20.8	310	21	US-09-761-288-4	Sequence 4, Appl
44	59	20.8	310	21	US-09-761-288-38	Sequence 38, Appl
45	59	20.8	310	21	US-09-761-288-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
PCT-US98-14613-142
; Sequence 142, Application PC/TUS9814613
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: P2011PCT
; CURRENT APPLICATION NUMBER: PCT/US98/14613
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/052,870
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-14613-142

Query Match 100.0%; Score 283; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRCVRHVLGIGLIVLNKLYFHKNMYPSPKLSQQEAFLEFFLLKKNPLTICS 54
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Db 1 MRRCVRHVLGIGLIVLNKLYFHKNMYPSPKLSQQEAFLEFFLLKKNPLTICS 54
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RESULT 2

APPLICANT: Rosen et al.
TITLE OF INVENTION: 64 Human Secreted Proteins

; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 25.88; Score 73; DB 1; Length 85;
Best Local Similarity 30.58; Pred. No. 0.67; Indels 14; Gaps 2;
Matches 18; Conservative 11; Mismatches 16; Indels 14; Gaps 2;

Qy 1 MRRC-----VRHVLGIGLIVKLNLYFKNSWPSKLSFQAEFLFFILKNPLTLC 53
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RESULT 6
US-09-764-874-6555
; Sequence 6555, Application US/09764874
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010
; CURRENT APPLICATION NUMBER: US/09764,874
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
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; PRIOR APPLICATION NUMBER: 60/180,628
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Query Match 25.8%; Score 73; DB 21; Length 85;
Best Local Similarity 30.5%; Pred. No. 0.67;
Matches 18; Conservative 11; Mismatches 16; Indels 14; Gaps 2;

QY 1 MRRC-----VRHVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLKNPILTC 53
DB 6 LRECLLMTCTIRTAGRMHILKSLQF-----GQIKNPQEQFAVFLVVKVPILFC 56

RESULT 7
US-09-809-391-362
; Sequence 362, Application US/09809391
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 362
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-362

Query Match 22.8%; Score 64.5; DB 22; Length 132;

Best Local Similarity 30.5%; Pred. No. 0.67;
Matches 18; Conservative 11; Mismatches 16; Indels 14; Gaps 2;

QY 1 MRRC-----VRHVLGIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLKNPILTC 53
DB 6 LRECLLMTCTIRTAGRMHILKSLQF-----GQIKNPQEQFAVFLVVKVPILFC 56

RESULT 7
US-09-809-391-362
; Sequence 362, Application US/09809391
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 362
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-362

Best Local Similarity 37.5%; Pred. No. 12;
Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps 5;

QY 1 MRRCVRH-VLIGLIVLKNLYFHKNMYPSPKLSFQEAFLFFLLIL 46
DB 1 MEHCLYHSHVGI-----NPYIHKNT-HPSINIMYMWDEQVNSFEREFVFFFLII 49

RESULT 8
US-09-882-171-362
; Sequence 362, Application US/09882171
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; Prior application number: 09/809,391
; Prior Filing Date: 2001-03-16
; Prior Application Number: 09/149,476
; Prior Filing Date: 1998-09-08
; Prior Application Number: PCT/US98/04493
; Prior Filing Date: 1998-03-06
; Prior Application Number: 60/040,162
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/040,333
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/038,621
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/040,626
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/040,334
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/040,336
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/040,163
; Prior Filing Date: 1997-03-07
; Prior Application Number: 60/047,600
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,615
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,597
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,502
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,633
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,583
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,617
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,618
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,503
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,592
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,581
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,584
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,500
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,587
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,492
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,598
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,613
; Prior Filing Date: 1997-05-23
; Prior Application Number: 60/047,582
; Prior Filing Date: 1997-05-23

;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,631
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,845
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,892
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/057,761
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/047,595
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,599
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,588
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,585
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,586
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,590
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,594
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,589
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,593
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/047,614
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/043,578
;	PRIOR FILING DATE:	1997-04-11
;	PRIOR APPLICATION NUMBER:	60/043,576
;	PRIOR FILING DATE:	1997-04-11
;	PRIOR APPLICATION NUMBER:	60/047,501
;	PRIOR FILING DATE:	1997-05-23
;	PRIOR APPLICATION NUMBER:	60/043,670
;	PRIOR FILING DATE:	1997-04-11
;	PRIOR APPLICATION NUMBER:	60/056,632
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,664
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,876
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,881
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,909
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,875
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,862
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,887
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/056,908
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/048,964
;	PRIOR FILING DATE:	1997-06-06
;	PRIOR APPLICATION NUMBER:	60/057,650
;	PRIOR FILING DATE:	1997-09-05
;	PRIOR APPLICATION NUMBER:	60/056,884
;	PRIOR FILING DATE:	1997-08-22
;	PRIOR APPLICATION NUMBER:	60/057,669
;	PRIOR FILING DATE:	1997-09-05
;	PRIOR APPLICATION NUMBER:	60/049,610

QY 1 MRRCVRH-VLIGLIVLKNIYFKHSMYP-----PKLSSEQEAFI-FFFLIL 46
| | : | | | | | | | | | | : | | | |
Db 1 MEHCPLYSHVGI-----NPYIKHT-NPSPINIMVWDEQVNSFREFVPFFELII 49

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01330-218

Query Match      22.6%; Score 64; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 9,6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
      |||||: :| :|: |||:|
Db 13 LIVLKSFFFFKDSLTPSPRL 32

RESULT 12
PCT-US01-01339-4675
; Sequence 4675, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4675
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01339-4675

Query Match      22.6%; Score 64; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 9,6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
      |||||: :| :|: |||:|
Db 13 LIVLKSFFFFKDSLTPSPRL 32

RESULT 13
PCT-US01-01339-5353
; Sequence 5353, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5353
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01339-5353

Query Match      22.6%; Score 64; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 9,6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
      |||||: :| :|: |||:|
Db 13 LIVLKSFFFFKDSLTPSPRL 32

RESULT 14
US-09-764-891-4675
; Sequence 4675, Application US/09764891
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4675
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-4675

Query Match 22.6%; Score 64; DB 21; Length 89;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
||||: |||: |||:
Db 13 LIVLKSFFFFKDSLTSPRL 32

RESULT 15
US-09-764-891-5353
; Sequence 5353, Application US/09764891
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5353
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-5353

Query Match 22.6%; Score 64; DB 21; Length 89;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNMYPSPKL 32
||||: |||: |||:
Db 13 LIVLKSFFFFKDSLTSPRL 32

Search completed: November 21, 2002, 13:45:40
Job time : 143 secs


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QY      11  IGLIVLKNLYFHKNSMYPSPKLSFSQEAFLFFFLIKNPL  50
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      236  VGLDSLESFYDNKLVKVPQLAQKVPNLKFLDLINKNPI  275

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RESULT 8

US-10-131-824A-512
; Sequence 512, Application US/10131824A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C126

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 512

; LENGTH: 716

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-131-824A-512

Query Match 18.4%; Score 52; DB 6; Length 716;

Best Local Similarity 32.5%; Pred. No. 24;

Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 11 IGLIVLKNLYPHKSNMYPSPKLSFQEAFLFFFLILKNPL 50

Db 236 VGLDSLSLSFYDNKLVKVPQLAQKVPNLKFLDLNKNPI 275

RESULT 9

US-10-131-826A-512

; Sequence 512, Application US/10131826A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128

; CURRENT APPLICATION NUMBER: US/10/131,826A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 512

; LENGTH: 716

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-131-826A-512

Query Match 18.4%; Score 52; DB 6; Length 716;

Best Local Similarity 32.5%; Pred. No. 24;

Matches 13; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 11 IGLIVLKNLYPHKSNMYPSPKLSFQEAFLFFFLILKNPL 50

Db 236 VGLDSLSLSFYDNKLVKVPQLAQKVPNLKFLDLNKNPI 275

RESULT 10

US-10-131-829A-512

; Sequence 512, Application US/10131829A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K

1	APPLICANT:	Gao,Wei-Qiang	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
2	APPLICANT:	Gerritsen,Mary E.	
3	APPLICANT:	Goddard,Audrey	
4	APPLICANT:	Godowski,Paul J.	
5	APPLICANT:	Gurney,Austin L.	
6	APPLICANT:	Sherwood,Steven	
7	APPLICANT:	Smith,Victoria	
8	APPLICANT:	Stewart,Timothy A.	
9	APPLICANT:	Tumas,Daniel	
10	APPLICANT:	Watanabe,Colin K	
11	APPLICANT:	Wood,William	
12	APPLICANT:	Zhang, Zemin	
13	TITLE OF INVENTION:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	
14	TITLE OF INVENTION:	ACIDS ENCODING THE SAME	
15	FILE REFERENCE:	P3330RIC85	
16	CURRENT APPLICATION NUMBER:	US/10/127,829A	
17	CURRENT FILING DATE:	2002-10-15	
18	PRIOR APPLICATION NUMBER:	60/049911	
19	PRIOR FILING DATE:	1997-06-18	
20	PRIOR APPLICATION NUMBER:	60/056974	
21	PRIOR FILING DATE:	1997-08-26	
22	PRIOR APPLICATION NUMBER:	60/059113	
23	PRIOR FILING DATE:	1997-09-17	
24	PRIOR APPLICATION NUMBER:	60/059115	
25	PRIOR FILING DATE:	1997-09-17	
26	PRIOR APPLICATION NUMBER:	60/059117	
27	PRIOR FILING DATE:	1997-09-17	
28	PRIOR APPLICATION NUMBER:	60/059122	
29	PRIOR FILING DATE:	1997-09-17	
30	PRIOR APPLICATION NUMBER:	60/059184	

0:

Search completed: November 21, 2002, 13:45:57
Job time : 12 secs

A:Gene: MTH331
A:Start codon: GTG
C:Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase
Query Match 21.2%; Score 60; DB 2; Length 221;
Best Local Similarity 30.9%; Pred. No. 3.2; Indels 24; Gaps 3;
Matches 21; Conservative 8; Mismatches 15;
QY 2 RCRCVHHVLGIGL-----IVLKNLYFHKNMYPSPKLSLSPQEAR- 39
DB 153 RRARHILEGLNYSQFELEAEFMFKSLARGLKIVEVPITYRKRS--DEPKLSSTDFGFK 210
QY 40 LFFFLILK 47
: : : : :
DB 211 IFFTVILE 218

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A:Gene: CESP.T03D3.10
A:Map position: 5
A:Introns: 109/3; 235/3; 269/3; 326/2

Query Match      20.7%; Score 58.5; DB 2; Length 394;
Best.local Similarity 30.8%; Pred.No. 9;
Matches 10; Conservative 11; Mismatches 18; Indels 7; Gaps 3;

QY    6 RHVIGLIGLVKNLYF-HKNSWYPGPKLSFSQ--EAPLFELILKNPLTCS 54
      ||| |||| :| | | | | | | | | | | | | | | | | |
DB    20 RHLIVGLRLLSEVLASKQTFFENKTRTFQFMNLEDWIYL---PSTFCA 67
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RESULT 6
AD0114 conserved hypothetical protein YPO0932 [Imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AD0114
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice,
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bar-
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB00001; MUID:21470413; PMID:11586360
A:Accession: AD0114
A:Accession: AD0114

probable membrane protein
N:Alternate names: hypothetical protein G9596
C:Species: *Saccharomyces cerevisiae*
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C:Update: Saccharomyces cerevisiae
C:Accession: S64628; S64630
R:Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64611
A:Accession: S64628
A:Molecule type: DNA
A:Residues: 1-153 <VOE>

J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28263
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-177 <FAO>
A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97649.1; PID:g4049689
C:Genetics:
A:Note: MSV102

Query Match 19.8%; Score 56; DB 2; Length 177;
Best Local Similarity 36.4%; Pred. No. 8.3;
Matches 12; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 18 NLVYFHNSMYPSPKLSSTFQEAFLFFFLILKNPL 50
| : | | : | : | : | : | : | : | : | : |
Db 137 DLIFCKNIITINPTNNYKKALNFYLDKKNKL 169

RESULT 10
T27463
hypothetical protein Y87G2A.k - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27463
R:White, S.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20371
A:Accession: T27463
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-321 <WIL>
A:Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54485.1; CESP:Y87G2A.k
C:Genetics:
A:Gene: CESP:Y87G2A.k
A:Introns: 29/1; 89/1; 189/1; 299/3

Query Match 19.8%; Score 56; DB 2; Length 321;
Best Local Similarity 32.4%; Pred. No. 15;
Matches 11; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 17 KNLYFHNSMYPSPKLSSTFQEAFLFFFLILKNPL 50
| : | | | | : | : | : | : | : | : | : |
Db 7 KLLFHSNGPKPTKFKFKLTQQILYFNRRKNPI 40

RESULT 11
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; et al.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835; PMID:7851893
A:Accession: A55735
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:I31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 19.8%; Score 56; DB 2; Length 378;
Best Local Similarity 32.6%; Pred. No. 18;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLIVLNLYFHNSMYPSPKLSSTFQEAFLFFFLIL 46
ph 69 CFVGLGNGLVILYVFVKRLKYMTDTYLLNLAVADILFLIL 111
| : | | | | | : | : | : | : | : | : | : |

RESULT 12
T51858
branched-chain alpha keto-acid dehydrogenase E1 alpha chain [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C:Accession: T51858
R:Mooney, B.P.; Miernyk, J.A.; Randall, D.D.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z25485
A:Accession: T51858
A:Status: partial; prev. translated from cDNA; 100%

A: Molecule type: mRNA
A: Residues: 1-472 <MOO>
A: Cross-references: EMBL:AF077955; PIDN:AAC69851.1
C: Superfamily: pyruvate dehydrogenase (lipocaine) alpha chain; thiamin pyrophosphate-binding

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QY      5  VRHVLGIGLTLVLKLVYFHKNMSYPSKLSLQFAFLFFFLILKNPLT  51
      :|| :| :|| :|| :| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db     14  LRHNLNLSTILIKRDYSHRPIFTTSQLSS--TAYLSPFGSLRHST  58

RESULT  13
A86347
branched-chain alpha keto-acid dehydrogenase E1-alpha subunit [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: A86347

```

R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816–820, 2000

A.A. Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitli, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yang, C.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86347
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <STO>
A:Cross-references: GB:AE005172; NID:g9454571; PIDN:AAF87894.1; GSPDB:GN00141

A:Map position: 1
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin

Matches 16; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

RESULT 14
AC1185
B. subtilis YtB protein homolog lmo0883 [imported] - Listeria monocytogenes (strain EGD
Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Accession: AC1185
Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H.
J.; Jones, L.M.; Karst, U.
Science 294 849-852, 2001
Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Ma

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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:42:31 ; Search time 10 Seconds
(without alignments)
84.572 Million cell updates/sec

Title: US-09-776-724A-142
Perfect score: 283
Sequence: 1 MRRCVHVGLGILVKNLY.....FOEAFLEFFLLKNPLTLC 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_PEP.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB_PEP.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB_PEP.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_PEP.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_PEP.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB_PEP.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	59	20.8	260	10	US-09-761-288-35
2	59	20.8	260	10	US-09-761-288-35
3	59	20.8	304	10	US-09-747-835A-58
4	59	20.8	310	10	US-09-761-288-4
5	59	20.8	310	10	US-09-761-288-38
6	59	20.8	310	10	US-09-761-288-67
7	59	20.8	310	10	US-09-761-288-89
8	58.5	20.7	612	8	US-08-910-386A-2
9	55.5	19.6	91	12	US-10-001-879-160
10	52.5	18.6	96	10	US-09-925-301-1300
11	52.5	18.6	216	10	US-09-745-763-4
12	52.5	18.6	1025	8	US-08-910-386A-7
13	52	18.4	310	10	US-09-761-288-22
14	52	18.4	310	10	US-09-761-288-24
15	52	18.4	310	10	US-09-761-288-64
16	52	18.4	372	10	US-09-804-156-15
17	52	18.4	372	10	US-09-946-633-7
18	52	18.4	384	9	US-09-945-249-8
19	52	18.4	714	10	US-09-803-589-7
					Sequence 35, Appl
					Sequence 36, Appl
					Sequence 58, Appl
					Sequence 4, Appl
					Sequence 38, Appl
					Sequence 89, Appl
					Sequence 2, Appl
					Sequence 160, Appl
					Sequence 1300, Appl
					Sequence 4, Appl
					Sequence 7, Appl
					Sequence 22, Appl
					Sequence 24, Appl
					Sequence 64, Appl
					Sequence 15, Appl
					Sequence 7, Appl
					Sequence 8, Appl
					Sequence 7, Appl

20	51.5	18.2	318	10	US-09-801-368-252	Sequence 252, Appl
21	51	18.0	193	10	US-09-815-242-4983	Sequence 4983, Appl
22	51	18.0	206	10	US-09-811-284-189	Sequence 189, Appl
23	50.5	17.8	63	10	US-09-864-761-37449	Sequence 37449, Appl
24	50	17.7	103	10	US-09-764-864-1448	Sequence 1448, Appl
25	50	17.7	160	10	US-09-764-864-1020	Sequence 1020, Appl
26	50	17.7	189	10	US-09-764-878-162	Sequence 162, Appl
27	50	17.5	655	10	US-09-815-242-13946	Sequence 13946, Appl
28	49.5	17.5	96	10	US-09-905-243-11	Sequence 11, Appl
29	49	17.3	66	10	US-09-764-887-265	Sequence 265, Appl
30	49	17.3	117	9	US-09-949-842-17	Sequence 17, Appl
31	49	17.3	315	10	US-09-978-249-9	Sequence 9, Appl
32	49	17.3	413	10	US-09-771-161A-178	Sequence 178, Appl
33	49	17.3	422	10	US-09-771-161A-269	Sequence 269, Appl
34	49	17.3	422	10	US-09-771-161A-270	Sequence 270, Appl
35	49	17.3	426	9	US-09-909-650A-24	Sequence 24, Appl
36	49	17.3	541	12	US-10-047-676A-11	Sequence 11, Appl
37	49	17.3	581	12	US-10-139-876-18	Sequence 18, Appl
38	49	17.3	837	12	US-10-052-586-454	Sequence 454, Appl
39	48.5	17.1	292	10	US-09-886-055-315	Sequence 315, Appl
40	48.5	17.1	313	10	US-09-886-055-115	Sequence 115, Appl
41	48.5	17.1	700	10	US-09-841-132-345	Sequence 345, Appl
42	48.5	17.1	1751	10	US-09-841-132-445	Sequence 445, Appl
43	48.5	17.1	1751	10	US-09-841-132-594	Sequence 594, Appl
44	48.5	17.1	1752	10	US-09-841-132-180	Sequence 180, Appl
45	48	17.0	105	10	US-09-740-668A-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-09-761-288-35
; Sequence 35, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spyttek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152)..(165)
; OTHER INFORMATION: Wherein Xaa is any amino acid.

US-09-761-288-35

Query Match 20.8%; Score 59; DB 10; Length 260;

Best Local Similarity 30.4%; Pred. No. 1.2;

Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVHVIGIGLIVLKNLYFHKNMYPSPKLSFQAEFLFFFLILKNPL---TLCS 54

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Db 188 RTCFSLCVGLVGYGTATIMYVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 240

RESULT 2

US-09-761-288-36

; Sequence 36, Application US/09761288

; Patent No. US20020065405A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Prayaga, Sudhirdas

; APPLICANT: Taupier, Raymond J

; APPLICANT: Mishra, Vishnu

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberky

; APPLICANT: Li, Li

; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam

; FILE REFERENCE: 15966-638

; CURRENT APPLICATION NUMBER: US/09761,288

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 60/177,839

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/176,134

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/175,989

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/218,324

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/220,253

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/220,590

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-761-288-36

Query Match 20.8%; Score 59; DB 10; Length 260;

Best Local Similarity 30.4%; Pred. No. 1.2;

Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVHVIGIGLIVLKNLYFHKNMYPSPKLSFQAEFLFFFLILKNPL---TLCS 54

| | | | | : : : : : | : | | | | : | | : | |

Db 188 RTCFSLCVGLVGYGTATIMYVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 240

RESULT 3

US-09-747-835A-58

; Sequence 58, Application US/09747835A

; Patent No. US20020146692A1

; GENERAL INFORMATION:

; APPLICANT: Yamazaki, Victoria

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Zhou, Ping

; APPLICANT: Wang, Dunrui

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Asundi, Vinod

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-L

; FILE REFERENCE: HYS-37CIP

; CURRENT APPLICATION NUMBER: US/09747,835A

; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: US 09/729,739

; PRIOR FILING DATE: 2000-12-04

; PRIOR APPLICATION NUMBER: US 09/653,450

; PRIOR FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: US 09/620,312

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: US 09/598,042

; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: US 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 58

; LENGTH: 304

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-747-835A-58

Query Match 20.8%; Score 59; DB 10; Length 304;

Best Local Similarity 30.4%; Pred. No. 1.4;

Matches 17; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 2 RRCVHVIGIGLIVLKNLYFHKNMYPSPKLSFQAEFLFFFLILKNPL---TLCS 54

| | | | | : : : : : | : | | | | : | | : | |

Db 238 RTCFSLCVGLVGYGTATIMYVGPYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290

RESULT 4

US-09-761-288-4

; Sequence 4, Application US/09761288

; Patent No. US20020065405A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Prayaga, Sudhirdas

; APPLICANT: Taupier, Raymond J

; APPLICANT: Mishra, Vishnu

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberky

; APPLICANT: Li, Li

; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding

; FILE REFERENCE: 15966-638

; CURRENT APPLICATION NUMBER: US/09761,288

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 60/177,839

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 60/176,134

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/175,989

; PRIOR FILING DATE: 2000-01-13

; PRIOR APPLICATION NUMBER: 60/218,324

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/220,253

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: 60/178,191

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227

; PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/220,590

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 310

; TYPE: PRT

; ORGANISM: Homo sapiens


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; APPLICANT: Caferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Cancer
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-160

Query Match 19.6%; Score 55.5; DB 12; Length 91;
Best Local Similarity 38.5%; Pred. No. 1.1;
Matches 15; Conservative 7; Mismatches 12; Indels 5

QY 14 IVLKLYPHKSNWYPSKLSFQAEAFLEFFFLKNPITL 52
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DDB 58 VVIHLYFF--LIPSKSLTS--ATFIFFLLLLHHP CFL 91

RESULT 10
US-09-925-301-1300
; Sequence 1300, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1300
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1300

Query Match 18.6%; Score 52.5; DB 10; Length 96;
Best Local Similarity 35.0%; Pred. No. 2.8;
Matches 14; Conservative 5; Mismatches 16; Indels 5

QY 17 KNLYPHKSNWY--PSPKLSFQAEAFLEFFFLKNPITLC 53
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DDB 18 KNCFLHPCGAYSSEPSQOCL--CFLYFCISIRFL LLLC 55

RESULT 11
US-09-745-763-4
; Sequence 4, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM

```


NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-745-763-4

Query Match 18.6%; Score 52.5; DB 10; Length 216;
Best Local Similarity 25.9%; Pred. No. 7;
Matches 14; Conservative 14; Mismatches 21; Indels 5; Gaps 1;
QY 1 MRRCVRHVLGVLKLVKLYFKHNSMYPSPKLSFQEAFLFFLLKKNPLTLC 54
Db 27 MATVCSILGVCLVMPINVEDNSL-----LNWKEAFGYMTVMAGLTALS 75

RESULT 12
US-910-386A-7
Sequence 7, Application US/08910386A
Patent No. US2002092041A1
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scot
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,386A
FILING DATE: 13-AUG-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-0589500S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1025 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-386A-7
Query Match 18.6%; Score 52.5; DB 8; Length 1025;
Best Local Similarity 36.2%; Pred. No. 42;
Matches 17; Conservative 6; Mismatches 19; Indels 5; Gaps 2;
QY 1 MRRCVRHVLGVLKLVKLYFKHNSM--YPSF--KLSSFQEAFLFF 42
Db 163 LRGMIPREIGASLKHLNLYKNGLSGEIPSAIGNLTSLOEFDLSF 209

RESULT 13
US-09-761-288-22
Sequence 22, Application US/09761288
Patent No. US20020065405A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberky
APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/177,839
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/176,134
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/175,989
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-288-22

Query Match 18.4%; Score 52; DB 10; Length 310;
Best Local Similarity 29.6%; Pred. No. 12;
Matches 16; Conservative 8; Mismatches 24; Indels 6; Gaps 2;
QY 4 CVRHVLGVLKLVKLYFKHNSMYPSPKLSFQEAFLFFLLKKNPL--TLCS 54
Db 240 CFSHLCVIGLFGYGTAIMYGPYGNPK---EQKYLHLLHSLFNPMLNPLICS 290
RESULT 14
US-09-761-288-24

Search completed: November 21, 2002, 13:46:13
Job time : 10 secs

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RESULT 15
US-09-761-288-64
/ Sequence 64, Application US/09761288
/ Patent No. US20020065405A1
/ GENERAL INFORMATION:
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Prayaga, Sudhirdhas
/ APPLICANT: Taupier, Raymond J
/ APPLICANT: Mishra, Vishnu
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: SpYtek, Kimberky
/ APPLICANT: Li, Li
/ TITLE OF INVENTION: No. US20020065405A1
/ FILE REFERENCE: 15966-638
/ CURRENT APPLICATION NUMBER: US/09/761-288-64
/ CURRENT FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: 60/177,839
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 60/176,134
/ PRIOR FILING DATE: 2000-01-14
/ PRIOR APPLICATION NUMBER: 60/175,989
/ * PRIOR FILING DATE: 2000-01-13
/ PRIOR APPLICATION NUMBER: 60/218,324
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 60/220,253
/ PRIOR FILING DATE: 2000-07-24

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: APPLICANT: Li, Li
:
: TITLE OF INVENTION: No. US20020065405A1e1 Polypeptides and Nucleic Acids Encoding Sam
:
: FILE REFERENCE: 15966-638
:
: CURRENT APPLICATION NUMBER: US/09/761,288
:
: CURRENT FILING DATE: 2001-01-16
:
: PRIOR APPLICATION NUMBER: 60/177,839
:
: PRIOR FILING DATE: 2000-01-25
:
: PRIOR APPLICATION NUMBER: 60/176,134
:
: PRIOR FILING DATE: 2000-01-14
:
: PRIOR APPLICATION NUMBER: 60/175,989
:
: PRIOR FILING DATE: 2000-01-13
:
: *PRIOR APPLICATION NUMBER: 60/218,324
:
: PRIOR FILING DATE: 2000-07-14
:
: PRIOR APPLICATION NUMBER: 60/220,253
:
: PRIOR FILING DATE: 2000-07-24

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:51 ; Search time 14 Seconds
(without alignments)
113.488 Million cell updates/sec

Title: US-09-776-724A-142

Perfect score: 283

Sequence: 1 MRRCVHVHVLGILVILKNLY.....FOEAFLEFFLILKNPLTLC5 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2.6/prodata/1/1aa/5A_COMB.pep:.*
2: /cgn2.6/prodata/1/1aa/5B_COMB.pep:.*
3: /cgn2.6/prodata/1/1aa/6A_COMB.pep:.*
4: /cgn2.6/prodata/1/1aa/6B_COMB.pep:.*
5: /cgn2.6/prodata/1/1aa/PCTUS_COMB.pep:.*
6: /cgn2.6/prodata/1/1aa/backfiles1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	64.5	22.8	132	4	US-09-149-476-362
2	58.5	20.7	673	4	US-09-134-001C-4480
3	56	19.8	359	1	US-08-153-848-24
4	56	19.8	359	3	US-09-299-843A-24
5	56	19.8	359	4	US-09-088-337B-24
6	56	19.8	359	5	PCT-US93-11153-24
7	56	19.8	378	3	US-09-299-843A-66
8	56	19.8	378	4	US-09-088-337B-66
9	56	19.8	472	4	US-09-108-020-12
10	55.5	19.6	554	4	US-08-180-371-2
11	55.5	19.6	554	5	PCT-US92-05707-2
12	52.5	18.6	1012	2	US-08-475-891A-4
13	52.5	18.6	1025	2	US-08-567-375-4
14	52.5	18.6	1025	2	US-08-587-680A-4
15	52	18.4	358	1	US-08-153-848-19
16	52	18.4	358	3	US-09-299-843A-19
17	52	18.4	358	4	US-09-088-337B-19
18	52	18.4	358	5	PCT-US93-11153-19
19	52	18.4	361	3	US-08-902-294-2
20	52	18.4	361	3	US-09-178-637-2
21	52	18.4	378	1	US-08-383-750-2
22	52	18.4	378	1	US-08-383-751A-2
23	52	18.4	378	3	US-08-153-848-15
24	52	18.4	378	3	US-08-352-678-2
25	52	18.4	378	3	US-09-299-843A-15
26	52	18.4	378	4	US-09-251-545-1
27	52	18.4	378	4	US-09-045-583-49

28	52	18.4	378	4	US-09-088-337B-15	Sequence 15, Appl
29	52	18.4	378	4	US-09-534-185-49	Sequence 49, Appl
30	52	18.4	378	5	PCT-US93-09636-2	Sequence 2, Appl
31	52	18.4	378	5	PCT-US93-11153-15	Sequence 15, Appl
32	52	18.4	410	1	US-08-153-848-7	Sequence 7, Appl
33	52	18.4	410	3	US-09-299-843A-7	Sequence 7, Appl
34	52	18.4	410	4	US-09-088-337B-7	Sequence 7, Appl
35	52	18.4	410	5	PCT-US93-11153-7	Sequence 7, Appl
36	51.5	18.2	3200	2	US-08-477-451-8	Sequence 8, Appl
37	51	18.0	415	4	US-09-198-956-6	Sequence 6, Appl
38	51	18.0	415	4	US-09-670-141-6	Sequence 6, Appl
39	51	18.0	422	4	US-09-025-580-3	Sequence 3, Appl
40	51	18.0	600	3	US-08-904-871-3	Sequence 3, Appl
41	51	18.0	1098	3	US-08-726-214-10	Sequence 10, Appl
42	51	18.0	1261	4	US-09-473-716-2	Sequence 2, Appl
43	51	18.0	2523	1	US-08-185-432-18	Sequence 18, Appl
44	51	18.0	2523	4	US-08-899-232-3	Sequence 3, Appl
45	51	18.0	2890	4	US-09-413-814-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-149-476-362
; Sequence 362, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23


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; EARLIER APPLICATION NUMBER: 60/057,569
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      22.8%; Score 64.5; DB 4; Length 132;
Best Local Similarity 37.5%; Pred. No. 0.057;
Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps 5;

QY 1 MRCVRH-VLIGLIVLKNLYFKHNSMYP-----PKLSFQEAFL-FFFLIL 46
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Db 1 MECHLSVHGI-----NPYHKNT-HPSINYMWDEQVNSFRFVPFFFLII 49
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
US-09-134-001C-4480
; Sequence 4480, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4480
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4480

Query Match      20.7%; Score 58.5; DB 4; Length 673;
Best Local Similarity 32.3%; Pred. No. 2.9;
Matches 20; Conservative 7; Mismatches 14; Indels 21; Gaps 4;

QY 6 RHVL-----GIGLVLK---NLYFHKNMYPSPKLS-----FQEAFLFFFLIL 46
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Db 21 RHIVFISVISILFGIEYILLSLTNTIYF--NEHHPKISAIIGIVFMTMLLFILY 78
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 47 KN 48
   |
Db 79 AN 80
   |

RESULT 3
US-08-153-848-24
; Sequence 24, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
```

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; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804e1 and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-24

Query Match      19.8%; Score 56; DB 1; Length 359;
Best Local Similarity 32.6%; Pred. No. 3.2;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIVLKNLYFHKNMYPSPKLSFQEAFLFFFLIL 46
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Db 49 CFVGLLGNGLVILTYIFKRLKTMTDTYLLNLAVADILFLIL 91
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-09-299-843A-24
; Sequence 24, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
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; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/377,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-66

Query Match 19.8%; Score 56; DB 3; Length 378;
Best Local Similarity 32.6%; Pred. No. 3.4;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLVILKLYFHKNMYPSPKLSFQFAFLFFLL 46
| : || || : || : | : | : | : | : |
Db 69 CFVGLGNGLVILTYIFKRLKMTDTYLLNLAVADILFLIL 111

RESULT 8
US-09-088-337B-66
; Sequence 66, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Attorney: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B

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; FILING DATE: 01-JUN-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-088-337B-66

Query Match 19.8%; Score 56; DB 4; Length 378;
Best Local Similarity 32.6%; Pred. No. 3.4;
Matches 14; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 4 CVRHVLGIGLVILKLYFHKNMYPSPKLSFQFAFLFFLL 46
| : || || : || : | : | : | : | : |
Db 69 CFVGLGNGLVILTYIFKRLKMTDTYLLNLAVADILFLIL 111

RESULT 9
US-09-108-020-12
; Sequence 12, Application US/09108020A
; Patent No. 6143561
; GENERAL INFORMATION:
; APPLICANT: Randall, Douglas D.
; APPLICANT: Johnston, Mark L.
; APPLICANT: Miernyk, Jan A.
; APPLICANT: Luethy, Michael H.
; APPLICANT: Mooney, Brian P.
; TITLE OF INVENTION: USE OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND
; TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO
; TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS
; FILE REFERENCE: UMO 1482
; CURRENT APPLICATION NUMBER: US/09/108,020A
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 60/051,291
; EARLIER FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 60/055,255
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/076,544
; EARLIER FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-108-020-12

Query Match 19.8%; Score 56; DB 4; Length 472;
Best Local Similarity 34.0%; Pred. No. 4.5;
Matches 16; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 5 VRHVLGIGLVILKLYFHKNMYPSPKLSFQFAFLFFLLKNPLT 51
| : || || : || : | : | : | : | : |
Db 14 LHNHNLSTILIKRDYSHRPFIYTSQLSS--TAYLSFPGSLRHST 58

RESULT 10

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US-08-180-371-2
; Sequence 2, Application US/08180371
; Patent No. 6254861
; GENERAL INFORMATION:
; APPLICANT: Choudhury, Chandra
; TITLE OF INVENTION: Hematopoietic Growth Factor Derived
; TITLE OF INVENTION: from T Lymphocytes and Methods of Use Therefor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,371
; FILING DATE: 12-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 906866
; FILING DATE: 01 July 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gruber, Lewis S.
; REGISTRATION NUMBER: 30,060
; REFERENCE/DOCKET NUMBER: 27620/31668
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
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; MOLECULE TYPE: protein
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Best Local Similarity 26.0%; Pred. No. 6.4;
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RESULT 11
; Sequence 2, Application PC/TUS9205707
; GENERAL INFORMATION:
; APPLICANT: Choudhury, Chandra
; TITLE OF INVENTION: Hematopoietic Growth Factor Derived from
; TITLE OF INVENTION: T Lymphocytes and Methods of Use Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05707
; FILING DATE: 19920707
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gruber, Lewis S.
; REGISTRATION NUMBER: 30,060
; REFERENCE/DOCKET NUMBER: 27620/30933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
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; SEQUENCE CHARACTERISTICS:
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; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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Best Local Similarity 26.0%; Pred. No. 6.4;
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RESULT 12
US-08-475-891A-4
; Sequence 4, Application US/08475891A
; Patent No. 5859339
; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yuang
; TITLE OF INVENTION: Procedures and Materials for Conferring
; TITLE OF INVENTION: Disease Resistance in Plants
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,891A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,375
; FILING DATE: 17-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 02370-058910US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1012 amino acids
; TYPE: amino acid
; STRANDEDNESS:

Search completed: November 21, 2002, 13:43:12
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 13:40:47 ; Search time 35 Seconds
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Scoring table: BLOSUM62
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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73	25.8	85	22	AB117898	Human nervous syst
3	64.5	22.8	132	19 AAW74772	Human secreted pro
4	64	22.6	89	22 AAM96017	Human reproductive
5	64	22.6	89	22 AAM96695	Human reproductive
6	64	22.6	89	22 AAU18865	Novel prostate gla
7	64	22.6	89	22 AAU18919	Novel prostate gla
8	60	21.2	99	22 AAU06321	Human polypeptide
9	59.5	21.0	237	21 AAG47243	Arabidopsis thalia
10	59.5	21.0	251	21 AAG47242	Arabidopsis thalia

11	59.5	21.0	307	21	AAG47241	Arabidopsis thalia
12	59	20.8	310	22	AAU05132	Human odorant rece
13	59	20.8	310	22	AAG71441	Human olfactory re
14	59	20.8	310	22	AAG71472	Human olfactory re
15	59	20.8	310	23	AAU91543	Human PHO1-F5D6 a
16	59	20.8	339	22	AAG72954	Human olfactory re
17	58.5	20.7	611	20	AAW93594	O. longistaminata
18	58.5	20.7	673	23	ABF39635	Staphylococcus epi
19	57.5	20.3	70	23	ABP51925	Human colon specif
20	57	20.1	72	21	AAG15836	Arabidopsis thalia
21	57	20.1	94	21	AAG15835	Arabidopsis thalia
22	57	20.0	125	22	AAO07863	Human polypeptide
23	56.5	20.0	95	22	AAO07862	Human polypeptide
24	56.5	20.0	122	22	AAO03290	Human polypeptide
25	56	19.8	359	15	AAK53747	Seven transmembran
26	56	19.8	359	19	AAW48728	Murine V31 seven t
27	56	19.8	359	21	AAE21691	Murine 7TM recepto
28	56	19.8	359	23	AAU91233	Mouse 7 transmembr
29	56	19.8	378	21	AAE21699	7TM receptor prote
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31	56	19.8	472	20	AAW88442	Arabidopsis branch
32	56	19.8	491	23	ABW47385	Listeria monocytog
33	55.5	19.6	103	22	AAO03045	Human polypeptide
34	55.5	19.6	134	22	AAO13437	Human polypeptide
35	55.5	19.6	172	23	ABW89059	Human polypeptide
36	55.5	19.6	554	14	AAK31930	Murine TC-CSF. Mu
37	55.5	19.6	554	14	AAK31932	Murine TC-CSF pept
38	55.5	19.6	554	22	AAE05133	Murine T cell-deri
39	55	19.4	59	22	AAW80894	Human haematologic
40	55	19.4	62	23	ABP00261	Human ORFX protein
41	55	19.4	199	22	AAU19189	Human G protein-co
42	54.5	19.3	200	21	AAQ28190	Arabidopsis thalia
43	54.5	19.3	228	21	AAQ28189	Arabidopsis thalia
44	54.5	19.3	312	21	AAQ28188	Arabidopsis thalia
45	54.5	19.3	1757	20	AAW84351	Murine ubiquitin-p

ALIGNMENTS

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AA101442
ID AA101442 standard; Protein; 54 AA.
AC AA101442;
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DT 18-MAY-1999 (first entry)
XX
DE Secreted protein encoded by gene 60 clone HOSDK95.
XX
KW Human; secreted protein; gene therapy; protein therapy; cancer; weight;
KW tumour; chromosome mapping; forensic; haematological disease; allergy;
KW inflammation; cell proliferation; viral infection; wound healing;
KW modulation; appetite; behaviour; food additive; preservative.
XX
OS Homo sapiens.
XX
XX
PN WO9903990-A1.
XX
XX
PD 28-JAN-1999.
XX
XX
PF 15-JUL-1998; 98WO-US14613.
XX
PR 18-AUG-1997; 97US-0056361.
PR 16-JUL-1997; 97US-0052661.
PR 16-JUL-1997; 97US-0052870.
PR 16-JUL-1997; 97US-0052871.
PR 16-JUL-1997; 97US-0052872.
PR 16-JUL-1997; 97US-0052873.
PR 16-JUL-1997; 97US-0052874.
PR 16-JUL-1997; 97US-0052875.
PR 22-JUL-1997; 97US-0053440.
PR 22-JUL-1997; 97US-0053441.

PR 22-JUL-1997; 97US-0053442.
 PR 18-AUG-1997; 97US-0055683.
 PR 18-AUG-1997; 97US-0055724.
 PR 18-AUG-1997; 97US-0055725.
 PR 18-AUG-1997; 97US-0055726.
 PR 18-AUG-1997; 97US-0055946.
 PR 18-AUG-1997; 97US-0055952.
 PR 18-AUG-1997; 97US-0055985.
 PR 18-AUG-1997; 97US-0055989.
 PR 18-AUG-1997; 97US-0056359.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Duan R, Feng P, Ferrie AM, Florence KA, Fouad J;
 PI Greene JM, Hu J, Ni J, Rosen CA, Ruben SM, Young PE;
 PI Yu G;
 XX
 XX WPI: 1999-132234/11.
 DR N-PSDB; AAX22270.
 DR
 DR
 XX
 PT New nucleic acids encoding secreted human proteins - potentially
 PT useful for treating and diagnosing diseases and identifying specific
 PT binding agents
 PT
 XX
 XX Claim 11; Page 233; 251pp; English.
 XX
 CC The invention relates to nucleic acid sequences (AAX22211 to AAX22282)
 CC encoding human secreted proteins (AAY01383 to AAY01454). The secreted
 CC protein gene sequences are deposited with the ATCC under deposit number
 CC ATCC 209138, 209139 or 209141. Host cells containing vectors comprising
 CC the nucleic acid sequences are used for the recombinant expression of
 CC the secreted proteins. The polynucleotide and amino acid sequences are
 CC useful for preventing, treating or ameliorating medical conditions e.g.
 CC by protein or gene therapy. Pathological conditions can be also diagnosed
 CC by determining the amount of the new polypeptides in a sample or by the
 CC presence of mutations in the new polynucleotides. The nucleic acid
 CC sequences, or its fragments, are useful for chromosome identification
 CC and mapping; as antisense and triplex-forming therapeutics; in gene
 CC therapy; for (forensic) identification of individuals; as molecular
 CC weight markers; to identify related sequences or specific mRNA; in
 CC preparation of oligomers and to raise anti-DNA antibodies. Antibodies are
 CC useful as immunoassay reagents (including for in vivo imaging) and
 CC therapeutically to inhibit or activate particular polypeptides. A very
 CC wide range of disorders may be treated with the polynucleotide and
 CC polypeptide sequences, e.g. autoimmune or haematological diseases,
 CC allergy, inflammation, cancer or other forms of cell proliferation, viral
 CC or other infections. The sequences may also be useful in wound healing,
 CC to modulate differentiation of embryonic stem cells, to modulate weight,
 CC appetite, behaviour etc. and as food additive or preservative. The
 CC present sequence represents a human secreted protein (see descriptor
 CC line for gene number and clone identification).
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 SQ Sequence 54 AA;

Query Match 100.0%; Score 283; DB 20; Length 54;
 Best Local Similarity 100.0%; Pred. No. 5.4e-34;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ID ABB17898 standard; Protein; 85 AA.
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 AC ABB17898;
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 XX 23-JAN-2002 (first entry)
 DT
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 DE Human nervous system related polypeptide SEQ ID NO 6555.
 XX

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 antiparkinsonian; antiskinning; antianaemic; antiarthritic; cancer;
 antirheumatic; hepatotropic; cerebroprotective; antinflammatory;
 antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 neurological disease; infection; nephrotropic; gene therapy; vaccine.
 XX Homo sapiens.
 XX
 XX WO200159063-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01334.
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 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
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 PR 26-JUL-2000; 2000US-0220963.
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 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
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 PR 01-SEP-2000; 2000US-0229344.
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 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
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 PR 08-SEP-2000; 2000US-0230438.
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XX PF 06-MAR-1998; 98WO-US04493.
XX PF 02-OCT-1997; 97US-0061060.
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PR PR 06-JUN-1997; 97US-0048974.
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PR 22-AUG-1997; 97US-0056882.
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PR 22-AUG-1997; 97US-0056893.
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PR 12-SEP-1997; 97US-0058785.
XX PA
XX (HUMA-) HUMAN GENOME SCI INC.
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Larleir DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI; 1998-506364/43.
DR N-PSDB; AAV59553.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
- useful for diagnosis and treatment of e.g. cancers, neurological
disorders, immune diseases, inflammation or blood disorders
Claim 1; Page 564-565; 721pp; English.
XX
XX This sequence represents a secreted human protein encoded by the nucleic
acid molecule designated Gene 43 from the human cDNA clone HSNBB14
(deposited as clone ATCC 97899 and ATCC 209045).
XX The gene can be used to generate fusion proteins by linking to the gene
to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
stability of the fused protein as compared to the human protein only.
XX The invention relates to 186 novel genes and their fragments (nucleic
acid sequences: AAV59511-V59812; amino acid sequences AAW4731-W75026)
XX which are useful for preventing, treating or ameliorating medical
conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 186
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAV59511 for described uses).
XX SQ Sequence 132 AA;
Query Match 22.8%; Score 64.5; DB 19; Length 132;
Best Local Similarity 37.5%; Pred. No. 0.21;
Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps 5;
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RESULT 4
AAM96017
ID AAM96017 standard; Protein; 89 AA.
XX
AC AAM96017;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4675.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy.
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
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PR 12-SEP-2000; 2000US-0231968.
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PR 08-NOV-2000; 2000US-0246613.
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PR 17-NOV-2000; 2000US-0249299.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
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 PR 06-DEC-2000; 2000US-0251479.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX
 DR WFL; 2001-465570/50.
 DR N-PSDB; AAL01987.

XX Isolated nucleic acid molecule encoding a reproductive system antigen
 PT is used in preventing, treating or ameliorating a medical condition -
 PT
 XX
 PS Claim 11; SEQ ID NO 4675; 1297pp + Sequence Listing; English.
 XX

CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a protein of the invention.
 XX
 XX Sequence 89 AA;

Query Match 22.6%; Score 64; DB 22; Length 89;
 Best Local Similarity 60.0%; Pred. No. 0.15;
 Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 13 LIVLKNLYFHKNMYPSPKL 32

Db 13 LIVLKSFFFFKSLTPSPRL 32

RESULT 5

AAM96695

ID AAM96695 standard; Protein; 89 AA.

XX
 AC AAM96695;

XX
 DT 21-NOV-2001 (first entry)

XX
 XX Human reproductive system related antigen SEQ ID NO: 5353.

XX
 DE Human reproductive system related antigen; reproductive system disorder;
 XX cancer; gene therapy.

XX
 KW Homo sapiens.

XX
 KW WO200153320-A2.

XX
 PN 02-AUG-2001.

XX
 PD 17-JAN-2001; 2001WO-US01339.

XX
 PF 31-JAN-2000; 2000US-0179065.

XX
 XX 04-FEB-2000; 2000US-0180628.

XX
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 XX 02-MAR-2000; 2000US-0186350.

XX
 XX 16-MAR-2000; 2000US-0189874.

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 XX 18-APR-2000; 2000US-0198123.

XX
 XX 19-MAY-2000; 2000US-0205515.

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PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2000US-02559678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465570/50.

Isolated nucleic acid molecule encoding a reproductive system antigen -
is used in preventing, treating or ameliorating a medical condition -

Disclosure; SEQ ID NO 5353; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a
number of human reproductive system related antigens. These can be used
in the prevention and treatment of reproductive system disorders,
including cancer. The present sequence is a protein of the invention.

SQ Sequence 89 AA;

Query Match 22.6%; Score 64; DB 22; Length 89;
Best Local Similarity 60.0%; Pred. NO. 0.15;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 13 LIVLKNLYFHKNSMYPSPKL 32
||||: :| |:| :|||:
Db 13 LIVLKSFFFFKDSLTPSRL 32

RESULT 6
AAU18865
ID AAU18865 standard; Protein; 89 AA.
XX
AC AAU18865;
XX
DT 21-NOV-2001 (first entry)
XX
DE Novel prostate gland antigen, Seq ID No 164.
XX
KW Human; neurotropic; neuroprotective; cytostatic; antiparkinsonian;
KW antianaemic; dermatological; immunosuppressive; antiinflammatory;
KW antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic;
KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;
KW prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;
KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;
KW reproductive system disorder; autoimmune disorder; urinary system;
KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;
KW blood-related disorder; hyperproliferative disorder; respiratory;
KW neurological disorder; endocrine disorder; inflammatory disorder;
KW liver disorder; wound healing; food preservative.
XX
OS Homo sapiens.
XX
PN WO200155447-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01330.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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 PR 20-OCT-2000; 2000US-0241826.
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 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
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 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2000US-0254097.
 PR 05-JAN-2001; 2000US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-476223/51.

N-PSDB; RAS30306.

Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia

Claim 1; SEQ ID No 164; 512pp; English.

The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, acute bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anemia), hyperproliferative disorders, urinary system disorders (glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Addison's disease), gastrointestinal disorders (inflammatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is

Query Match 22.6%; Score 64; DB 22; Length 89;

Best Local Similarity 60.0%; Pred. No. 0.15;

Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 13 LIVLKNLYFHKNMYPSPKL 32

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PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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FT SPYDER NA, NI NI,

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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides, the polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scentfingerprint or scent profile), which may be used to

Db 238 RTCFSHLCVIGLVGTAIIMVGPYGNPK---EQKKYLLLFHSLFNPLNPLICS 290

Search completed: November 21, 2002, 13:41:32
Job time : 37 secs

